

APPENDIX A: BLAST SEARCHES



tigr db

arabidopsis thaliana

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Arabidopsis thaliana Blast Search

BLASTN 2.0MP-WashU [10-May-2005] [linux26-i686-ILP32F64 2005-05-10T21:11:22]

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Reference: Gish, W. (1996-2005) <http://blast.wustl.edu>

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak protein similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= query_sequence **NGGGGAGGATN or NGCGGAGGCTN**
(11 letters)

WARNING: the maximum achievable score of 55 for gapped alignments in frame +1 is less than the gapped cutoff score gapS2 (=81).

WARNING: the maximum achievable score of 55 for gapped alignments in frame -1 is less than the gapped cutoff score gapS2 (=81).

Database: ATH1.cdna

28,952 sequences; 43,903,363 total letters.

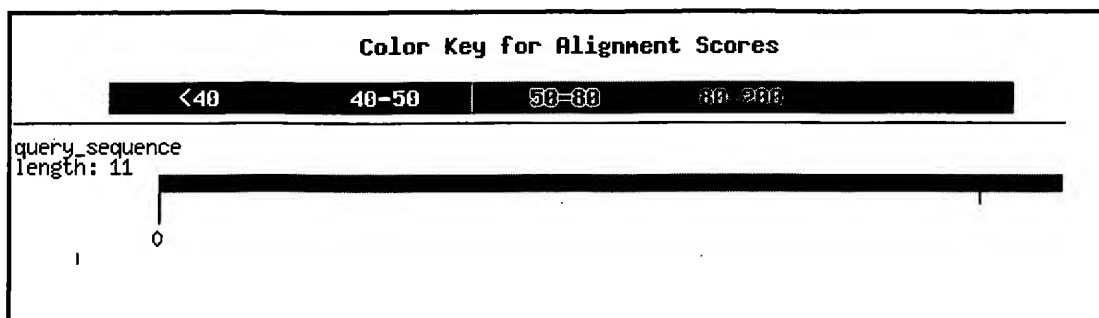
Searching....10....20....30....40....50....60....70....80....90....100% done

	High	Smallest
	Score	Sum
Sequences producing High-scoring Segment Pairs:	Probability	
	P(N)	N

*** NONE ***

Distribution of Blast Hits on the Query Sequence

Mouse-over to show name and scores. Click to show alignments.



Parameters:

```

filter=dust
E=10
B=20
V=20
cpus=1
-o blastn-annotation_dbs_ATH1.cdna-15763-1155058214

ctxfactor=2.00
    
```

Query			-----	As Used		-----	Computed		-----
Strand	MatID	Matrix name	Lambda	K	H	Lambda	K	H	
+1	0	+5,-4	0.192	0.182	0.357	same	same	same	
		Q=10,R=10	0.104	0.0151	0.0600	n/a	n/a	n/a	
-1	0	+5,-4	0.192	0.182	0.357	same	same	same	
		Q=10,R=10	0.104	0.0151	0.0600	n/a	n/a	n/a	

Query											
Strand	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2	
+1	0	11	11	9.6	134	11	n/a	73	0.048	51	
								134	0.046	81	
-1	0	11	11	9.6	134	11	n/a	73	0.048	51	
								134	0.046	81	

Statistics:

```

Database: /usr/local/db/euk/pub/a_thaliana/annotation_dbs/ATH1.cdna
Title: ATH1.cdna
Posted: 12:55:19 PM EST Feb 9, 2004
Created: 11:06:03 AM EST Feb 9, 2004
Format: XDF-1
# of letters in database: 43,903,363
# of sequences in database: 28,952
# of database sequences satisfying E: 0
No. of states in DFA: 8 (8 KB)
Total size of DFA: 9 KB (2050 KB)
Time to generate neighborhood: 0.00u 0.00s 0.00t Elapsed: 00:00:00
No. of threads or processors used: 1
Search cpu time: 0.02u 0.01s 0.03t Elapsed: 00:00:00
Total cpu time: 0.02u 0.01s 0.03t Elapsed: 00:00:00
Start: Tue Aug 8 13:30:14 2006 End: Tue Aug 8 13:30:14 2006
WARNINGS ISSUED: 2
    
```

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Please report problems to blast@tigr.org